

MBI-0032.ST25.txt
SEQUENCE LISTING

<110> Broun, Pierre
<120> Method for Modifying a Biosynthetic Pathway
<130> MBI-0032
<160> 8
<170> PatentIn version 3.0
<210> 1
<211> 1239
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (6)..(1091)
<223> G993

```

<400> 1
caaat atg gaa tac agc tgt gta gac gac agt agt aca acg tca gaa tct      50
      Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser
        1             5             10             15

ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa      98
Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
              20             25             30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc     146
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
              35             40             45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag     194
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
              50             55             60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct     242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
              65             70             75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg     290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
              80             85             90             95

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc     338
Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
              100            105            110

gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct     386
Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
              115            120            125

caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct     434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
              130            135            140

```

aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu 145 150 155	482
ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser 160 165 170 175	530
ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg 180 185 190	578
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu 195 200 205	626
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu 210 215 220	674
ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly 225 230 235	722
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg 240 245 250 255	770
tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp 260 265 270	818
agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys 275 280 285	866
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys 290 295 300	914
gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn 305 310 315	962
att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys 320 325 330 335	1010
gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys 340 345 350	1058
tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt ttttttggtt Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu 355 360	1111
ttttttcttca atttgtttct cttttttcaa ttttttgtat tgaaatgaca agttgtaaat	1171

taggacaaga caagaaaaaa tgacaactag acaaaatagt ttttgtttaa aaaaaaaaaa 1231
 aaaaaaaaaa 1239

<210> 2
 <211> 361
 <212> PRT
 <213> Arabidopsis thaliana

<400> 2

Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser Leu
 1 5 10 15

Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
 20 25 30

Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
 35 40 45

Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
 50 55 60

Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
 65 70 75 80

Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
 85 90 95

Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
 100 105 110

Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
 115 120 125

Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys
 130 135 140

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
 145 150 155 160

Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
 165 170 175

Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
 180 185 190

Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
195 200 205

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
210 215 220

Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
225 230 235 240

Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
245 250 255

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
260 265 270

Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
275 280 285

Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
290 295 300

Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
305 310 315 320

Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
325 330 335

Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
340 345 350

Lys Lys Gln Ala Ile Ile Asn Ile Leu
355 360

<210> 3
<211> 1226
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (111)..(989)
<223> G1845

<400> 3
aagacataat tttctctgtt ttccctagctc tctcctctca aattcttcca ttgctctctg

ttttggcaaa tcgtgaactg ccacgtcttt aaggcatcag tgaagcaaag atg gac	116
Met Asp	
1	
ttt gac gag gag cta aat ctt tgt att acg aaa ggt aaa aat gtt gat	164
Phe Asp Glu Glu Leu Asn Leu Cys Ile Thr Lys Gly Lys Asn Val Asp	
5 10 15	
cat tct ttt gga gga gaa gct tct tcc acg tcc cca aga tct atg aag	212
His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser Met Lys	
20 25 30	
aaa atg aag agt cct agt cgt cct aaa ccc tat ttc caa tcc tct tct	260
Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser Ser Ser	
35 40 45 50	
tct cct tat tcg tta gag gct ttc cct ttt tct ctc gat cca aca ctt	308
Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro Thr Leu	
55 60 65	
cag aat cag caa caa caa ctc gga tca tac gtt ccg gta ctt gag caa	356
Gln Asn Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu Glu Gln	
70 75 80	
cga caa gac ccg aca atg caa ggc cag aag caa atg atc tcc ttt agt	404
Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser Phe Ser	
85 90 95	
cct caa caa caa caa cag cag cag cag tat atg gcc cag tac tgg agt	452
Pro Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr Trp Ser	
100 105 110	
gac aca ttg aat ctg agt cca aga gga aga atg atg atg atg atg agc	500
Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met Met Ser	
115 120 125 130	
caa gaa gct gtt caa cct tac atc gca acg aag ctg tac aga gga gtg	548
Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg Gly Val	
135 140 145	
aga caa cgt caa tgg gga aaa tgg gtc gca gag atc cgt aag cca cga	596
Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys Pro Arg	
150 155 160	
agc agg gca cgt ctt tgg ctt ggt acc ttt gat aca gct gaa gaa gct	644
Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala	
165 170 175	
gcc atg gcc tac gac cgc caa gcc ttc aaa tta cga ggc cac agc gca	692
Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His Ser Ala	
180 185 190	
aca ctg aat ttc ccg gag cat ttt gtg aat aag gaa agc gag ctg cat	740
Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu Leu His	
195 200 205 210	
gat tca aac tcg tcg gat cag aaa gaa cct gaa acg cca cag cca agc	788
Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln Pro Ser	
215 220 225	

MBI-0032.ST25.txt

gag gtt aac ttg gag agc aag gaa cta ccg gtg att gat gtt ggg aga 836
Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val Gly Arg
230 235 240

gag gaa ggt atg gct gag gca tgg tac aat gcc att aca tcg gga tgg 884
Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser Gly Trp
245 250 255

ggt cct gaa agt cct ctt tgg gat gat ttg gat agt tct cat cag ttt 932
Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His Gln Phe
260 265 270

tca tca gaa agc tca tct tct tct cct ctc tct tgt cct atg agg cct 980
Ser Ser Glu Ser Ser Ser Ser Pro Leu Ser Cys Pro Met Arg Pro
275 280 285 290

ttc ttt tga aaaagtttat aaaccacat tgtgtgtgtag gttatagttt 1029
Phe Phe

agggttatgc tcattggcat ttggatggag gcaatttttg tgatctccca ttccaccaca 1089

tatcagtcac tatatgtgtc taccttttct ctgtatttct atcattatca ttgtttttat 1149

tatgtgtctg tatgtgtttc cctattgcta catacataga tgcctctttt gttcaaaaaa 1209

aaaaaaaaaa aaaaaaa 1226

<210> 4
<211> 292
<212> PRT
<213> Arabidopsis thaliana

<400> 4

Met Asp Phe Asp Glu Glu Leu Asn Leu Cys Ile Thr Lys Gly Lys Asn
1 5 10 15

Val Asp His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser
20 25 30

Met Lys Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser
35 40 45

Ser Ser Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro
50 55 60

Thr Leu Gln Asn Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu
65 70 75 80

Glu Gln Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser
85 90 95

Phe Ser Pro Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr
100 105 110

Trp Ser Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met
115 120 125

Met Ser Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg
130 135 140

Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys
145 150 155 160

Pro Arg Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu
165 170 175

Glu Ala Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His
180 185 190

Ser Ala Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu
195 200 205

Leu His Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln
210 215 220

Pro Ser Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val
225 230 235 240

Gly Arg Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser
245 250 255

Gly Trp Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His
260 265 270

Gln Phe Ser Ser Glu Ser Ser Ser Ser Pro Leu Ser Cys Pro Met
275 280 285

Arg Pro Phe Phe
290

<210> 5
<211> 845
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (89)..(673)

<223> G1386

<400> 5

aattttatatt ccttctctca aatcttccca ccaaaaatta actctttcgt tcacactaag 60

tcccttttaa aagaaaatat cccaatta atg gaa cgt gac gac tgc cgg aga 112
Met Glu Arg Asp Asp Cys Arg Arg
1 5

ttt cag gac tcg ccg gcg cag acg acg gag aga aga gtg aaa tat aaa 160
Phe Gln Asp Ser Pro Ala Gln Thr Thr Glu Arg Arg Val Lys Tyr Lys
10 15 20

cca aag aag aaa aga gcc aaa gat gat gat gat gag aaa gtt gtt tcg 208
Pro Lys Lys Lys Arg Ala Lys Asp Asp Asp Asp Glu Lys Val Val Ser
25 30 35 40

aag cat cca aat ttt cga ggt gtc aga atg aga caa tgg gga aaa tgg 256
Lys His Pro Asn Phe Arg Gly Val Arg Met Arg Gln Trp Gly Lys Trp
45 50 55

gtg tcc gaa atc aga gag cca aaa aag aaa tca aga atc tgg ctc ggt 304
Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile Trp Leu Gly
60 65 70

act ttc tcc acg gcg gag atg gcg gcg cgt gct cac gac gtg gca gct 352
Thr Phe Ser Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala
75 80 85

tta gcc atc aaa ggc ggt tct gca cat ctc aac ttc ccg gag ctc gct 400
Leu Ala Ile Lys Gly Gly Ser Ala His Leu Asn Phe Pro Glu Leu Ala
90 95 100

tat cac ctc cct aga cca gct agt gcc gac cct aaa gac atc caa gct 448
Tyr His Leu Pro Arg Pro Ala Ser Ala Asp Pro Lys Asp Ile Gln Ala
105 110 115 120

gcc gcc gcc gca gct gca gcc gct gtg gcc att gac atg gat gta gag 496
Ala Ala Ala Ala Ala Ala Ala Ala Val Ala Ile Asp Met Asp Val Glu
125 130 135

acg tct tcg ccg tcg cca tct ccc aca gtt acg gaa acg tca tct ccg 544
Thr Ser Ser Pro Ser Pro Ser Pro Thr Val Thr Glu Thr Ser Ser Pro
140 145 150

gct atg ata gca ctc tcc gac gac gcg ttc tcc gat ctt cct gat ctc 592
Ala Met Ile Ala Leu Ser Asp Asp Ala Phe Ser Asp Leu Pro Asp Leu
155 160 165

ttg ctc aac gtg aac cat aac atc gat ggc ttc tgg gac tct ttt ccc 640
Leu Leu Asn Val Asn His Asn Ile Asp Gly Phe Trp Asp Ser Phe Pro
170 175 180

tat gaa gaa ccc ttc ctc tct caa agt tac tag aaactcaaaa ctatgtcgtt 693
Tyr Glu Glu Pro Phe Leu Ser Gln Ser Tyr

185 190
 tttgtatgta tttttgtcat gtgaccatgt tttgacgtcg aaaatcaccc ggataatcca 753
 aattgtatga tttattaatg gttgatgatt ttctttgtgt ggaacaatgt gtatgatacg 813
 taatcaaaag ttcaaaaaaa aaataaaaaa aa 845

<210> 6
 <211> 194
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6

Met Glu Arg Asp Asp Cys Arg Arg Phe Gln Asp Ser Pro Ala Gln Thr
 1 5 10 15

Thr Glu Arg Arg Val Lys Tyr Lys Pro Lys Lys Lys Arg Ala Lys Asp
 20 25 30

Asp Asp Asp Glu Lys Val Val Ser Lys His Pro Asn Phe Arg Gly Val
 35 40 45

Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys
 50 55 60

Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Ser Thr Ala Glu Met Ala
 65 70 75 80

Ala Arg Ala His Asp Val Ala Ala Leu Ala Ile Lys Gly Gly Ser Ala
 85 90 95

His Leu Asn Phe Pro Glu Leu Ala Tyr His Leu Pro Arg Pro Ala Ser
 100 105 110

Ala Asp Pro Lys Asp Ile Gln Ala Ala Ala Ala Ala Ala Ala Ala
 115 120 125

Val Ala Ile Asp Met Asp Val Glu Thr Ser Ser Pro Ser Pro Ser Pro
 130 135 140

Thr Val Thr Glu Thr Ser Ser Pro Ala Met Ile Ala Leu Ser Asp Asp
 145 150 155 160

Ala Phe Ser Asp Leu Pro Asp Leu Leu Leu Asn Val Asn His Asn Ile
 165 170 175

Asp Gly Phe Trp Asp Ser Phe Pro Tyr Glu Glu Pro Phe Leu Ser Gln
180 185 190

Ser Tyr

<210> 7
<211> 891
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (59)..(646)
<223> G872

<400> 7
ccggaacag aatccaattc aaccaaaccg aatcgaaccg aaccggagtt tttatcca 58

atg gtg aag caa gcg atg aag gaa gag gag aag aag aga aac acg gcg 106
Met Val Lys Gln Ala Met Lys Glu Glu Lys Lys Arg Asn Thr Ala
1 5 10 15

atg cag tca aag tac aaa gga gtg agg aag agg aaa tgg gga aaa tgg 154
Met Gln Ser Lys Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp
20 25 30

gta tcg gag atc aga ctt cca cac agc aga gaa cga att tgg tta ggc 202
Val Ser Glu Ile Arg Leu Pro His Ser Arg Glu Arg Ile Trp Leu Gly
35 40 45

tct tac gac act ccc gag aag gcg gcg cgt gct ttc gac gcc gct caa 250
Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln
50 55 60

ttt tgt ctc cgc ggc ggc gat gct aat ttc aat ttc cct aat aat cca 298
Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
65 70 75 80

ccg tcg atc tcc gta gaa aag tcg ttg acg cct ccg gag att cag gaa 346
Pro Ser Ile Ser Val Glu Lys Ser Leu Thr Pro Pro Glu Ile Gln Glu
85 90 95

gct gct gct aga ttc gct aac aca ttc caa gac att gtc aag gga gaa 394
Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu
100 105 110

gaa gaa tcg ggt tta gta ccc gga tcc gag atc cga cca gag tct cct 442
Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro
115 120 125

tct aca tct gca tct gtt gct aca tcg acg gtg gat tat gat ttt tcg 490
Ser Thr Ser Ala Ser Val Ala Thr Ser Thr Val Asp Tyr Asp Phe Ser
130 135 140

MBI-0032.ST25.txt

ttt ttg gat ttg ctt ccg atg aat ttc ggg ttt gat tcc ttc tcc gac 538
Phe Leu Asp Leu Leu Pro Met Asn Phe Gly Phe Asp Ser Phe Ser Asp
145 150 155 160

gac ttc tct ggc ttc tcc ggt ggt gat cga ttt aca gag att tta ccc 586
Asp Phe Ser Gly Phe Ser Gly Gly Asp Arg Phe Thr Glu Ile Leu Pro
165 170 175

atc gaa gat tac gga gga gag agt tta tta gat gaa tct ttg att ctt 634
Ile Glu Asp Tyr Gly Gly Glu Ser Leu Leu Asp Glu Ser Leu Ile Leu
180 185 190

tgg gat ttt tga attcccaaac ataatatattt tttagagcga actgtgagat 686
Trp Asp Phe
195

tttccttggga gtcattggaga aatctggaga ttttttgttaa cacggagctc caatgacccg 746

ggaattttcctt tcgttttcgga tccgaatttg atgtggatca tattcacacc tatatttttt 806

catttttttg ttgtaaagaa aaatcggata agattctagt aataaatgtt aaaagtccat 866

ttcattaaaa aaaaaaaaaa aaaaa 891

<210> 8
<211> 195
<212> PRT
<213> Arabidopsis thaliana

<400> 8

Met Val Lys Gln Ala Met Lys Glu Glu Glu Lys Lys Arg Asn Thr Ala
1 5 10 15

Met Gln Ser Lys Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp
20 25 30

Val Ser Glu Ile Arg Leu Pro His Ser Arg Glu Arg Ile Trp Leu Gly
35 40 45

Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln
50 55 60

Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
65 70 75 80

Pro Ser Ile Ser Val Glu Lys Ser Leu Thr Pro Pro Glu Ile Gln Glu
85 90 95

Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu
100 105 110

MBI-0032.ST25.txt

Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro
 115 120 125

Ser Thr Ser Ala Ser Val Ala Thr Ser Thr Val Asp Tyr Asp Phe Ser
 130 135 140

Phe Leu Asp Leu Leu Pro Met Asn Phe Gly Phe Asp Ser Phe Ser Asp
 145 150 155 160

Asp Phe Ser Gly Phe Ser Gly Gly Asp Arg Phe Thr Glu Ile Leu Pro
 165 170 175

Ile Glu Asp Tyr Gly Gly Glu Ser Leu Leu Asp Glu Ser Leu Ile Leu
 180 185 190

Trp Asp Phe
 195